



RAW SEQUENCE LISTING DATE: 10/03/2000
PATENT APPLICATION: US/09/271,584 TIME: 16:25:14

```
Input Set : A:\salt seq listing.txt
Output Set: N:\CRF3\10032000\I271584.raw
```

4 <110> APPLICANT: BLUMWALD, Eduardo
5 APSE, Maris
6 SNEDDEN, Wayne
7 AHARON, Gilad
9 <120> TITLE OF INVENTION: GENETIC ENGINEERING SALT TOLERANCE IN CROP PLANTS
11 <130> FILE REFERENCE: 1110/0039
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/271,584
14 <141> CURRENT FILING DATE: 1999-03-18
16 <150> PRIOR APPLICATION NUMBER: US 60/078,474
17 <151> PRIOR FILING DATE: 1998-04-01
19 <150> PRIOR APPLICATION NUMBER: US 60/116,111
20 <151> PRIOR FILING DATE: 1999-01-15
22 <160> NUMBER OF SEQ ID NOS: 37
24 <170> SOFTWARE: PatentIn Ver. 2.1, Word 97

Does Not Comply
Corrected Diskette Needed

see pp. 1, 2

ERRORED SEQUENCES

```

2247 <210> SEQ ID NO: 37
2248 <211> LENGTH: 30
2249 <212> TYPE: DNA
2250 <213> ORGANISM: Synthetic
2252 <220> FEATURE:
2253 <223> OTHER INFORMATION: Page 55 - Primer
2255 <400> SEQUENCE: 37
2257 cgcgtcgaca tgttggttc tctagtgtcg
E--> 2258 1
E--> 2262 37/37

```

Extraneous material at end of file must be deleted. It is causing an invalid base count error

09/271, 584

p. 2
RECEIVE

<210> 23
<211> 378
<212> DNA
<213> Oryza sativa

<220>
<223> Figure 8(c)

<400> 23

caagaagcta tacattggaa ggcattctac tgaccgtgag gttgccctta tgatgctcat 60
ggcttacctt tcatatatgc tggctgagtt gctagatttg agcggcattc tcaccgtatt 120
cttctgtggt attgtaatgt cacattacac ttggcataac gtcacagaga gttcaagagt 180
tacaacaaag cacgcatttg caactctgtc cttcattgct gagacttttc tcttctgtta 240
tgttgggatg gatgcattgg atattgaaaa atgggaattt nccagtgaca gacctg^{na}aa 300
atccatt^{ng}g gtaagctcaa ttttgctagg gattggttcc tgattggaag ngctgctttt 360
naattcccc tggtggtc 378

Missing mandatory <220> to <223>
features to explain "n's" in the
sequence. See # 10 on Error Summary
Sheet.

This error
is also
indicated in

sequences

24, 25, 26, 27,
and 28.

Please check
the listing and
correct.

VERIFICATION SUMMARY

DATE: 10/03/2000

PATENT APPLICATION: US/09/271,584

TIME: 16:25:15

Input Set : A:\salt seq listing.txt

Output Set: N:\CRF3\10032000\I271584.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1698 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1698 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1698 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23
L:1699 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1699 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
M:340 Repeated in SeqNo=23
L:1700 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1700 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1714 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1714 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1714 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24
L:1716 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1716 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
M:340 Repeated in SeqNo=24
L:1717 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1717 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1730 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1730 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1730 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
L:1731 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1731 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
M:340 Repeated in SeqNo=25
L:1735 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
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L:1758 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
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L:1775 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
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L:1775 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27
L:1794 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
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L:1794 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
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M:340 Repeated in SeqNo=28
L:1796 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
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L:1797 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:2258 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:37
M:254 Repeated in SeqNo=37
L:2262 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:2262 M:252 E: No. of Seq. differs, <211>LENGTH:Input:30 Found:31 SEQ:37